

RAW SEQUENCE LISTING

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Application Serial Number: 10/048,116B
Source: IFW16
Date Processed by STIC: 4/20/06

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IFW16

RAW SEQUENCE LISTING

DATE: 04/20/2006

PATENT APPLICATION: US/10/048,116B

TIME: 09:51:03

Input Set : A:\seq list.txt

Output Set: N:\CRF4\04202006\J048116B.raw

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3 <110> APPLICANT: CNRS
5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
6 FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
7 IMMUNE RESPONSES
9 <130> FILE REFERENCE: 1721-47
11 <140> CURRENT APPLICATION NUMBER: 10/048,116B
12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
15 <151> PRIOR FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: FR99/09862
18 <151> PRIOR FILING DATE: 1999-07-29
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1517
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
31 coding IAalpha(d)/Fc
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(1502)
37 <400> SEQUENCE: 1
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39 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
40 1 5 10
42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att 98
43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
44 15 20 25
46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct 146
47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
48 30 35 40
50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc 194
51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
52 45 50 55
54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt 242
55 Tyr Val Asp Leu Asp Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
56 60 65 70 75
58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct 290
59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
60 80 85 90
62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc 338

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63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64          95          100          105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct 386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68          110          115          120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc 434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72          125          130          135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc 482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76          140          145          150          155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc 530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80          160          165          170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att 578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84          175          180          185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa 626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88          190          195          200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act 674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92          205          210          215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag 722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96          220          225          230          235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa 770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100          240          245          250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc 818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104          255          260          265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg 866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108          270          275          280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc 914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112          285          290          295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc 962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116          300          305          310          315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa 1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120          320          325          330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act 1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124          335          340          345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt 1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser

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128          350          355          360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc 1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132          365          370          375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag 1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380          385          390          395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc 1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140          400          405          410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg 1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144          415          420          425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa 1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148          430          435          440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga 1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152          445          450          455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg 1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460          465          470          475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg 1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160          480          485          490
162 act ccg ggt aaa tgatgactcg acctg 1517
163 Thr Pro Gly Lys
164          495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
174 coding IAalpha(d)/Fc
176 <400> SEQUENCE: 2
177 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
178 1          5          10          15
180 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
181          20          25          30
183 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
184          35          40          45
186 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
187          50          55          60
189 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
190 65          70          75          80
192 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
193          85          90          95
195 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu

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196          100          105          110
198 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
199          115          120          125
201 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
202          130          135          140
204 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
205 145          150          155          160
207 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
208          165          170          175
210 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Ile Tyr Asp Cys Lys Val
211          180          185          190
213 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
214          195          200          205
216 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
217          210          215          220
219 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
220 225          230          235          240
222 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
223          245          250          255
225 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
226          260          265          270
228 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
229          275          280          285
231 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
232          290          295          300
234 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
235 305          310          315          320
237 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
238          325          330          335
240 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
241          340          345          350
243 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
244          355          360          365
246 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
247          370          375          380
249 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
250 385          390          395          400
252 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
253          405          410          415
255 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
256          420          425          430
258 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
259          435          440          445
261 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
262          450          455          460
264 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
265 465          470          475          480
267 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
268          485          490          495

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271 <210> SEQ ID NO: 3
272 <211> LENGTH: 1485
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence: coding region
278     of SEQ ID NO:1
280 <220> FEATURE:
281 <221> NAME/KEY: CDS
282 <222> LOCATION: (1)..(1485)
284 <400> SEQUENCE: 3
285 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc 48
286 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
287 1 5 10 15
289 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta 96
290 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
291 20 25 30
293 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag 144
294 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
295 35 40 45
297 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat 192
298 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
299 50 55 60
301 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc 240
302 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
303 65 70 75 80
305 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac 288
306 Phe Glu Pro Gln Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
307 85 90 95
309 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag 336
310 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
311 100 105 110
313 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag 384
314 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
315 115 120 125
317 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc 432
318 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
319 130 135 140
321 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat 480
322 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
323 145 150 155 160
325 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct 528
326 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
327 165 170 175
329 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg 576
330 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
331 180 185 190
333 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag 624
334 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu

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VERIFICATION SUMMARY

DATE: 04/20/2006

PATENT APPLICATION: US/10/048,116B

TIME: 09:51:04

Input Set : A:\seq list.txt

Output Set: N:\CRF4\04202006\J048116B.raw